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(1) GENERAL INFORMATION:

- (i) APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
Silvia, Christopher P.
- (ii) TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/254,590
(B) FILING DATE: 24-MAY-1999
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/026,451
(B) FILING DATE: 11-SEP-1996
- a¹ (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/040,052
(B) FILING DATE: 07-MAR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/045,233
(B) FILING DATE: 17-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US97/16033
(B) FILING DATE: 10-SEP-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Weber, Kenneth A.
(B) REGISTRATION NUMBER: 31,677
(C) REFERENCE/DOCKET NUMBER: 014210-000730US
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..561
- (D) OTHER INFORMATION: /note= "human small conductance, calcium-activated potassium channel protein 1 (hSK1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Pro Gly Pro Arg Ala Ala Cys Ser Glu Pro Asn Pro Cys Thr Gln
1           5           10           15

Val Val Met Asn Ser His Ser Tyr Asn Gly Ser Val Gly Arg Pro Leu
          20           25           30

Gly Ser Gly Pro Gly Ala Leu Gly Arg Asp Pro Pro Asp Pro Glu Ala
          35           40           45

Gly His Pro Pro Gln Pro Pro His Ser Pro Gly Leu Gln Val Val Val
          50           55           60

Ala Lys Ser Glu Pro Ala Arg Pro Ser Pro Gly Ser Pro Arg Gly Gln
65           70           75           80

Pro Gln Asp Gln Asp Asp Asp Glu Asp Asp Glu Glu Asp Glu Ala Gly
          85           90           95

Arg Gln Arg Ala Ser Gly Lys Pro Ser Asn Val Gly His Arg Leu Gly
          100          105          110

His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala
          115          120          125

Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Thr Glu Thr Glu
          130          135          140

Leu Ser Trp Gly Val Tyr Thr Lys Glu Ser Leu Tyr Ser Phe Ala Leu
          145          150          155          160

Lys Cys Leu Ile Ser Leu Ser Thr Ala Ile Leu Leu Gly Leu Val Val
          165          170          175

Leu Tyr His Ala Arg Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala
          180          185          190

Asp Asp Trp Arg Ile Ala Met Thr Cys Glu Arg Val Phe Leu Ile Ser
          195          200          205

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Leu Glu Leu Ala Val Cys Ala Ile His Pro Val Pro Gly His Tyr Arg
 210 215 220
 Phe Thr Trp Thr Ala Arg Leu Ala Phe Thr Tyr Ala Pro Ser Val Ala
 225 230 235 240
 Glu Ala Asp Val Asp Val Leu Leu Ser Ile Pro Met Phe Leu Arg Leu
 245 250 255
 Tyr Leu Leu Gly Arg Val Met Leu Leu His Ser Lys Ile Phe Thr Asp
 260 265 270
 Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Thr Phe Asn Thr
 275 280 285
 Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu
 290 295 300
 Leu Val Phe Ser Ile Ser Ser Trp Ile Ile Ala Ala Trp Thr Val Arg
 305 310 315 320
 Val Cys Glu Arg Tyr His Asp Lys Gln Glu Val Thr Ser Asn Phe Leu
 325 330 335
 Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly
 340 345 350
 Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr
 355 360 365
 Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala
 370 375 380
 Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met
 385 390 395 400
 Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val
 405 410 415
 Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Arg Leu Val Lys Lys
 420 425 430
 Pro Asp Gln Ala Arg Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala
 435 440 445
 Ile His Gln Ala Gln Lys Leu Arg Ser Val Lys Ile Glu Gln Gly Lys
 450 455 460
 Leu Asn Asp Gln Ala Asn Thr Leu Thr Asp Leu Ala Lys Thr Gln Thr
 465 470 475 480
 Val Met Tyr Asp Leu Val Ser Glu Leu His Ala Gln His Glu Glu Leu
 485 490 495
 Glu Ala Arg Leu Ala Thr Leu Glu Ser Arg Leu Asp Ala Leu Gly Ala
 500 505 510
 Ser Leu Gln Ala Leu Pro Gly Leu Ile Ala Gln Ala Ile Arg Pro Pro
 515 520 525

Pro Pro Pro Leu Pro Pro Arg Pro Gly Pro Gly Pro Gln Asp Gln Ala
 530 535 540

Ala Arg Ser Ser Pro Cys Arg Trp Thr Pro Val Ala Pro Ser Asp Cys
 545 550 555 560

Gly

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..580
- (D) OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 2 (rSK2)"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 135..462
- (D) OTHER INFORMATION: /note= "core region of rSK2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Cys Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn
 1 5 10 15

Leu Ser Ser Ser Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln
 20 25 30

Pro Leu Gln Pro Pro Ala Ser Val Val Gly Gly Gly Gly Ala Ser
 35 40 45

Ser Pro Ser Ala Ala Ala Ala Ala Ser Ser Ser Ala Pro Glu Ile Val
 50 55 60

Val Ser Lys Pro Glu His Asn Asn Ser Asn Asn Leu Ala Leu Tyr Gly
 65 70 75 80

Thr Gly Gly Gly Gly Ser Thr Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95

Gly Gly Gly Ser Gly His Gly Ser Ser Ser Gly Thr Lys Ser Ser Lys
 100 105 110

Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His Arg Arg Ala Leu
 115 120 125

Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met
 130 135 140

Phe Gly Ile Val Val Met Val Ile Glu Thr Glu Leu Ser Trp Gly Ala
 145 150 155 160
 Tyr Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu Lys Cys Leu Ile Ser
 165 170 175
 Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Val Tyr His Ala Arg
 180 185 190
 Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala Asp Asp Trp Arg Ile
 195 200 205
 Ala Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys Leu Glu Ile Leu Val
 210 215 220
 Cys Ala Ile His Pro Ile Pro Gly Asn Tyr Thr Phe Thr Trp Thr Ala
 225 230 235 240
 Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr Thr Ala Asp Val Asp
 245 250 255
 Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg
 260 265 270
 Val Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser
 275 280 285
 Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys
 290 295 300
 Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile
 305 310 315 320
 Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr
 325 330 335
 His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu
 340 345 350
 Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro Asn
 355 360 365
 Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly Ala
 370 375 380
 Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu Leu
 385 390 395 400
 Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln Leu
 405 410 415
 Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val Leu Arg Glu Thr Trp
 420 425 430
 Leu Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys Ile Asp His Ala Lys
 435 440 445
 Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg
 450 455 460

Ser Val Lys Met Glu Gln Arg Lys Leu Asn Asp Gln Ala Asn Thr Leu
 465 470 475 480
 Val Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr Asp Met Ile Ser Asp
 485 490 495
 Leu Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg Ile Val Thr Leu Glu
 500 505 510
 Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His Ala Leu Pro Gly Leu
 515 520 525
 Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp Phe Ile Glu Thr Gln
 530 535 540
 Met Glu Asn Tyr Asp Lys His Val Thr Tyr Asn Ala Glu Arg Ser Arg
 545 550 555 560
 Ser Ser Ser Arg Arg Arg Arg Ser Ser Ser Thr Ala Pro Pro Thr Ser
 565 570 575
 Ser Glu Ser Ser
 580

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..553
- (D) OTHER INFORMATION: /note= "N-terminally truncated form of rat small conductance, calcium-activated potassium channel protein 3 (rSK3)"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 109..436
- (D) OTHER INFORMATION: /note= "core region of rSK3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro Leu Ser Arg
 1 5 10 15
 Leu Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Pro Glu Gly Gln
 20 25 30
 Pro Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Ile Ile Ser
 35 40 45

Ser Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro Asn
 50 55 60
 Ala Thr His Asn His Gln His Ala Gly Thr Thr Ala Gly Ser Thr Thr
 65 70 75 80
 Phe Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly Tyr Lys Leu
 85 90 95
 Gly His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr
 100 105 110
 Ala Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr
 115 120 125
 Glu Leu Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe Ser Leu Ala
 130 135 140
 Leu Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile
 145 150 155 160
 Ile Ala Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile Asp Asn Gly
 165 170 175
 Ala Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Leu Tyr Ile
 180 185 190
 Ser Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu Tyr
 195 200 205
 Lys Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg
 210 215 220
 Ala Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg
 225 230 235 240
 Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr
 245 250 255
 Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn
 260 265 270
 Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val
 275 280 285
 Leu Leu Met Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val
 290 295 300
 Arg Val Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe
 305 310 315 320
 Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr
 325 330 335
 Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu
 340 345 350
 Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val
 355 360 365

Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe
 370 375 380

Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn
 385 390 395 400

Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys
 405 410 415

Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln
 420 425 430

Ala Ile His Gln Leu Arg Gly Val Lys Met Glu Gln Arg Lys Leu Ser
 435 440 445

Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met
 450 455 460

Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys
 465 470 475 480

Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe
 485 490 495

Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln
 500 505 510

Gln Leu Leu Thr Ala Phe Val Glu Ala Arg Gly Ile Ser Val Ala Val
 515 520 525

Gly Thr Ser His Ala Pro Pro Ser Asp Ser Pro Ile Gly Ile Ser Ser
 530 535 540

Thr Ser Phe Pro Glu Phe Leu Ile Phe
 545 550

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..458
 - (D) OTHER INFORMATION: /note= "rat small conductance,
 calcium-activated potassium channel
 protein 1 (rSK1)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser	Gly	Lys	Pro	Pro	Thr	Val	Ser	His	Arg	Leu	Gly	His	Arg	Arg	Ala
1				5					10					15	

Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly
 20 25 30
 Met Phe Gly Ile Val Val Met Val Thr Glu Thr Glu Leu Ser Trp Gly
 35 40 45
 Val Tyr Thr Lys Glu Ser Leu Cys Ser Phe Ala Leu Lys Cys Leu Ile
 50 55 60
 Ser Leu Ser Thr Val Ile Leu Leu Gly Leu Val Ile Leu Tyr His Ala
 65 70 75 80
 Arg Glu Ile Gln Leu Phe Leu Val Asp Asn Gly Ala Asp Asp Trp Arg
 85 90 95
 Ile Ala Met Thr Trp Glu Arg Val Ser Leu Ile Ser Leu Glu Leu Ala
 100 105 110
 Val Cys Ala Ile His Pro Val Pro Gly His Tyr Arg Phe Thr Trp Thr
 115 120 125
 Ala Arg Leu Ala Phe Ser Leu Val Pro Ser Ala Ala Glu Ala Asp Val
 130 135 140
 Asp Val Leu Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu Leu Ala
 145 150 155 160
 Arg Val Met Leu Leu His Ser Arg Ile Phe Thr Asp Ala Ser Ser Arg
 165 170 175
 Ser Ile Gly Ala Leu Asn Arg Val Thr Phe Asn Thr Arg Phe Val Thr
 180 185 190
 Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser
 195 200 205
 Ile Ser Ser Trp Ile Val Ala Ala Trp Thr Val Arg Val Cys Glu Arg
 210 215 220
 Tyr His Asp Lys Gln Glu Val Thr Ser Asn Phe Leu Gly Ala Met Trp
 225 230 235 240
 Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro
 245 250 255
 His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly
 260 265 270
 Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu
 275 280 285
 Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln
 290 295 300
 Leu Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val Leu Arg Glu Thr
 305 310 315 320
 Trp Leu Ile Tyr Lys His Thr Arg Leu Val Lys Lys Pro Asp Gln Ser
 325 330 335

Arg Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Ala
 340 345 350

Gln Lys Leu Arg Thr Val Lys Ile Glu Gln Gly Lys Val Asn Asp Gln
 355 360 365

Ala Asn Thr Leu Ala Asp Leu Ala Lys Ala Gln Ser Ile Ala Tyr Glu
 370 375 380

Val Val Ser Glu Leu Gln Ala Gln Gln Glu Glu Leu Glu Ala Arg Leu
 385 390 395 400

Ala Ala Leu Glu Ser Arg Leu Asp Val Leu Gly Ala Ser Leu Gln Ala
 405 410 415

Leu Pro Ser Leu Ile Ala Gln Ala Ile Cys Pro Leu Pro Pro Pro Trp
 420 425 430

Pro Gly Pro Ser His Leu Thr Thr Ala Ala Gln Ser Pro Gln Ser His
 435 440 445

Trp Leu Pro Thr Thr Ala Ser Asp Cys Gly
 450 455

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGCCGGGTC CCCGGGCGGC CTGC

24

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCACCCGCAG TCCGAGGGGG CCAC

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAGCAGCT GCAGGTACAA CGGG

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAGCTACTC TCAGATGAAG TTGG

24

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAGCTCCT GCAAATACAG CGGT

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTAGCAACTG CTTGAACTTG

20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCAGGGAAGC CCCCACCGT CAGT

24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCACCCACAG TCTGATGCCG TGGT

24

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1683
- (D) OTHER INFORMATION: /note= "human small conductance,
calcium-activated potassium channel
protein 1 (hSK1) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCGGGTC CCCGGGCGGC CTGCAGCGAG CCCAACCCCT GCACCCAGGT AGTCATGAAC

60

AGCCACAGCT ACAATGGCAG CGTGGGGCGG CCGCTGGGCA GCGGGCCGGG CGCCCTGGGA

120

CGAGACCCTC CGGACCCTGA GGCCGGCCAC CCCCCACAAC CCCCGCACAG CCCGGGGCCTC	180
CAGGTGGTAG TGGCCAAGAG TGAGCCAGCC CGGCCCTCAC CCGGCAGCCC CCGGGGGCAG	240
CCCCAGGACC AGGACGATGA CGAGGATGAT GAGGAAGATG AGGCCGGCAG GCAGAGAGCC	300
TCGGGGAAAC CCTCAAATGT GGGCCACCGC CTGGGCCACC GGC GGCGCT CTTCGAGAAG	360
CGGAAGCGCC TCAGCGACTA TGCCCTCATT TTCGGCATGT TTGGCATCGT CGTCATGGTG	420
ACGGAGACCG AGCTGTCCTG GGGGGTGTAC ACCAAGGAGT CTCTGTACTC ATTTCGACTC	480
AAATGCCTCA TGAGCCTCTC CACGGCCATC CTGCTGGGTC TCGTTGTCCT CTACCATGCC	540
CGGGAGATCC AGCTGTTCAT GGTGGACAAC GGGGCTGATG ACTGGCGCAT CGCCATGACC	600
TGCGAGCGCG TGTTCTCAT CTCGCTAGAG CTGGCAGTGT GCGCCATTCA CCCGGTGCCC	660
GGCCACTACC GCTTCACGTG GACGGCGCGG CTGGCCTTCA CGTACGCGCC CTCGGTGGCC	720
GAGGCCGACG TGGACGTGCT GCTGTCCATC CCCATGTTCC TGGCCTCTA CCTGCTGGGC	780
CGGGTGATGC TACTGCACAG CAAAATCTTC ACGGACGCCT CGAGCCGAG CATCGGGGCC	840
CTCAACAAGA TCACCTTCAA CACGCGCTTC GTCATGAAGA CACTCATGAC CATCTGCCCC	900
GGCACCCTGC TGCTGGTCTT CAGCATCTCC TCCTGGATCA TCGCAGCCTG GACCGTGCGC	960
GTCTGCGAGA GGTACCACGA CAAGCAGGAA GTGACCAGCA ACTTCCTGGG GGCCATGTGG	1020
CTGATTTCCA TCACCTTCCT CTCCATTGGC TACGGCGACA TGGTGCCCCA CACCTACTGC	1080
GGGAAGGGTG TGTGCCTGCT CACTGGCATC ATGGGAGCTG GCTGTACCGC GCTCGTGGTG	1140
GCTGTGGTGG CTCGGAAGCT GGAGCTCACC AAGGCTGAGA AGCACGTGCA CAACTTCATG	1200
ATGGACACTC AGCTCACCAA GCGGGTAAAA AACGCCGCTG CTAACGTTCT CAGGGAGACG	1260
TGGCTCATCT ACAAACATAC CAGGCTGGTG AAGAAGCCAG ACCAAGCCCG GGTTCGGAAA	1320
CACCAGCGTA AGTTCCTCCA AGCCATCCAT CAGGCTCAGA AGCTCCGAG TGTGAAGATC	1380
GAGCAAGGGA AGCTGAACGA CCAGGCTAAC ACGCTTACCG ACCTAGCCAA GACCCAGACC	1440
GTCATGTACG ACCTTGATC GGAGCTGCAC GCTCAGCACG AGGAGCTGGA GGCCCGCCTG	1500
GCCACCCTGG AAAGCCGCTT GGATGCGCTG GGTGCCTCTC TACAGGCCCT GCCTGGCCTC	1560
ATCGCCCAAG CCATACGCCC ACCCCCGCCT CCCCTGCCTC CCAGGCCCGG CCCC GGCCCC	1620
CAAGACCAGG CAGCCCGGAG CTCCCCCTGC CGGTGGACGC CCGTGGCCCC CTCGGACTGC	1680
GGG	1683

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1374
- (D) OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 1 (rSK1) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGGGAAGC CCCCACCGT CAGTCACCGC CTGGGCCACC GTAGGGCCCT CTTCGAGAAG	60
CGTAAACGAC TCAGTGAATA TGCACTCATC TTTGGCATGT TCGGGATTGT CGTCATGGTG	120
ACAGAAACAG AGCTGTCCTG GGGTGTGTAC ACCAAGGAGT CTCTGTGCTC ATTCGCCCTG	180
AAATGCCTAA TCAGCCTCTC CACTGTCATC CTGCTTGGCC TTGTCATCCT CTACCACGCC	240
CGAGAGATCC AGCTGTTCTT GGTGGACAAT GGTGCCGATG ACTGGCGCAT TGCCATGACG	300
TGGGAGCGAG TGTCCCTGAT CTCGCTGGAG TTGGCTGTGT GTGCCATCCA CCCAGTGCCT	360
GGCCACTACC GCTTCACATG GACGGCGCGG CTGGCCTTCT CCCTGGTGCC GTCAGCAGCC	420
GAGGCGGATG TGGATGTGCT TCTGTCCATC CCCATGTTTC TGCGCCTCTA TCTGCTGGCT	480
CGGGTCATGC TCCTGCACAG CCGCATCTTC ACGGACGCAT CCAGTCGCAG CATCGGAGCC	540
CTGAACCGTG TCACCTTCAA CACACGCTTT GTCACCAAGA CACTCATGAC CATCTGCCCT	600
GGCACCCTGC TGTGGTCTT CAGCATCTCC TCCTGGATCG TCGCTGCATG GACAGTGCAG	660
GTGTGTGAGA GGTACCATGA TAAACAGGAA GTGACCAGCA ACTTCCTGGG GGCCATGTGG	720
CTCATCTCCA TTACCTTCCT GTCCATCGGC TACGGGGACA TGGTGCCGCA CACCTACTGT	780
GGGAAGGGCG TGTGTCTGCT CACCGGCATC ATGGGAGCAG GCTGCACTGC ACTCGTGGTG	840
GCCGTCGTGG CCCGCAAGTT GGAACCTACC AAGGCTGAGA AACACGTGCA CAACCTCATG	900
ATGGACACAC AGCTCACCAA GCGGGTTAAA AACGCCGCTG CAAACGTTCT CAGGGAGACA	960
TGGCTCATCT ACAAACACAC CAGGCTAGTG AAGAAGCCAG ACCAAAGCCG GGTTCGGAAA	1020
CACCAGCGTA AGTTCCTTCA GGCCATCCAT CAGGCGCAGA AGCTCCGGAC TGTGAAGATT	1080
GAACAAGGGA AGGTGAATGA TCAGGCCAAC ACGCTGGCTG ACCTGGCCAA GGCACAGAGC	1140
ATCGCATATG AGGTGGTGTC GGAGCTGCAG GCCCAGCAGG AGGAGTTGGA GGCCCGTCTG	1200

GCTGCCCTGG AGAGCCGCCT GGATGTCCTA GGCGCCTCCC TGCAGGCCCT ACCAAGTCTC	1260
ATAGCCCAAG CCATATGCCC TCTACCACCA CCCTGGCCCG GGCCCAGTCA CCTGACCACA	1320
GCCGCCCAGA GCCCACAAAG CCACTGGCTG CCCACCACGG CATCAGACTG TGGG	1374

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1740
- (D) OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 2 (rSK2) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGTCCGC TCAGCAACTT GAGCTCGTCC	60
CGCCGGAACC TGCACGAGAT GGA CT CAGAG GCTCAGCCCC TGCAGCCCCC AGCGTCGGTT	120
G TAGGAGGAG GTGGTGGTGC GTCCTCCCCG TCTGCTGCCG CCGCCGCCTC ATCCTCAGCC	180
CCAGAGATCG TGGTGTCTAA GCCGGAGCAC AACAATTCTA ACAACCTGGC GCTCTACGGA	240
ACTGGCGGCG GAGGCAGCAC CGGAGGCGGC GCGGCGGCG GCGGCGGCGG CGGCGGCAGC	300
GGGCATGGCA GCAGCAGCGG CACTAAGTCC AGCAAAAAGA AGAACCAGAA CATCGGCTAT	360
AAGCTGGGCC ATCGGCGTGC CCTGTTTGAG AAGCGCAAGC GGCTCAGCGA CTATGCGCTC	420
ATCTTCGGCA TGTTCCGGCAT CGTGGTCATG GTCATCGAGA CCGAGCTGTC GTGGGGCGCC	480
TACGACAAGG CGTCGCTGTA TTCTTTAGCT CTGAAATGCC TTATCAGTCT CTCCACGATC	540
ATCCTGCTTG GTCTGATCAT CGTATACCAC GCCAGGGAAT TACAGTTATT CATGGTGGAC	600
AATGGAGCAG ATGACTGGAG AATAGCCATG ACTTATGAAC GTATTTTCTT CATCTGCTTG	660
GAAATACTGG TGTGTGCTAT TCATCCCATC CCTGGGAATT ATACGTTTAC ATGGACAGCC	720
CGGCTTGCCT TCTCCTATGC CCCTTCCACA ACCACTGCAG ACGTGGATAT TATTTTATCT	780
ATACCAATGT TCTTAAGACT CTATCTGATT GCCAGAGTCA TGCTATTACA TAGCAAACCTT	840
TTCACCGATG CCTCCTCTAG AAGCATTGGG GCACTTAATA AGATAAACTT CAATACGCGT	900
TTTGTTATGA AGACTTTAAT GACTATCTGC CCAGGAACTG TGCTCTTGGT TTTTAGTATC	960
TCGTTATGGA TAATTGCCGC ATGGACTGTC CGAGCTTGTC AAAGGTACCA TGATCAACAG	1020

GATGTCACTA GCAACTTCCT TGGAGCAATG TGGTTGATAT CAATAACTTT TCTCTCCATT	1080
GGTTATGGTG ACATGGTACC TAACACATAC TGTGGGAAAG GAGTCTGCTT GCTTACCGGA	1140
ATAATGGGTG CAGGTTGCAC AGCCTTGGTG GTAGCCGTAG TGGCAAGGAA GCTAGAACTT	1200
ACCAAAGCAG AAAAGCATGT GCACAATTTT ATGATGGATA CTCAGCTGAC CAAAAGAGTA	1260
AAAAACGCAG CCGCCAATGT ACTCAGGGAA ACGTGGTTAA TCTACAAAAA CACAAAGCTA	1320
GTGAAAAAGA TCGACCATGC AAAAGTAAGG AAGCATCAAC GGAAATTCTT ACAAGCTATT	1380
CATCAATTAA GAAGTGTGAA GATGGAACAG AGGAAACTGA ATGACCAAGC GAATACGCTA	1440
GTGGATCTGG CAAAGACCCA AGATATCATG TATGATATGA TTTCCGACTT AAATGTAAGG	1500
AGTGAAGACT TTGAGAAAAG GATCGTCACC CTGGAAACAA AATTAGAAAC TTTGATTGGT	1560
AGCATTTCATG CCCTCCCTGG GCTTATCAGC CAGACCATCA GACAGCAGCA AAGGGACTTC	1620
ATAGAGACAC AGATGGAGAA CTATGACAAG CATGTACCTT ACAATGCTGA GCGTTCCCGG	1680
TCCTCGTCCA GGAGGCGGCG GTCCTCCTCC ACAGCGCCAC CAACTTCATC TGAGAGTAGC	1740

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1659
- (D) OTHER INFORMATION: /note= "N-terminally truncated cDNA
for rat small conductance,
calcium-activated potassium channel
protein 3 (rSK3) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGAGCTCCT GCAAATACAG CGGTGGGGTC ATGAAGCCCC TCAGCCGCCT CAGCGCCTCT	60
CGGAGAAACC TTATCGAGGC CGAGCCTGAG GGCCAACCCC TCCAGCTCTT CAGTCCCAGC	120
AACCCCCCAG AGATTATCAT CTCCTCCAGG GAGGATAACC ATGCCACCA GACTCTGCTC	180
CATCACCCCA ACGCTACCCA CAACCACCAG CATGCCGGCA CCACTGCTGG CAGCACCACC	240
TTCCCCAAAG CCAACAAGCG GAAAAACCAA AACATTGGCT ATAAGCTGGG GCACAGGAGG	300
GCCCTGTTTG AAAAGAGAAA GCGACTGAGT GACTATGCTC TGATTTTGGG GATGTTTGGG	360
ATTGTTGTTA TGGTGATAGA GACCGAACTG TCTTGGGGTT TGTACTCAA GGATTCCATG	420

TTTTCGTTGG CCCTGAAATG CCTTATCAGT TTATCCACCA TCATCCTGCT TGGTTTGATC	480
ATCGCCTACC ACACAAGGGA AGTACAGCTC TTTGTGATCG ACAATGGTGC AGATGACTGG	540
CGGATAGCCA TGACCTATGA GCGCATCCTC TACATCAGCC TGGAGATGCT GGTGTGCGCC	600
ATCCACCCCA TTCCTGGAGA GTACAAGTTC TTCTGGACGG CACGCCTGGC CTTCTCCTAC	660
ACCCCTCTC GGGCAGAGGC TGACGTGGAC ATTATTCTGT CCATCCCCAT GTTCTTGCGC	720
CTATACCTGA TCGCCCGAGT CATGCTGCTA CATAGCAAGC TCTTCACGGA TGCCTCATCC	780
CGAAGCATCG GGGCCCTCAA CAAGATCAAC TTCAACACCC GATTTCGTCAT GAAGACGCTC	840
ATGACCATCT GCCCGGGCAC GGTGCTGCTA ATGTTTCAGCA TCTCTCTGTG GATCATCGCT	900
GCCTGGACTG TGAGAGTCTG TGAAAGGTAC CATGACCAGC AGGACGTAAC TAGTAACTTT	960
CTGGGTGCCA TGTGGCTCAT CTCCATCACG TTCCTTTCCA TTGGCTATGG GGACATGGTG	1020
CCCCACACAT ACTGTGGGAA AGGTGTCTGT CTTCTCACTG GCATCATGGG TGCAGGCTGC	1080
ACTGCCCTCG TGGTAGCTGT GGTGCCCCG AAGCTCGAAC TCACCAAAGC AGAGAAGCAT	1140
GTGCACAAC TCATGATGGA CACTCAGCTC ACCAAACGGA TCAAGAACGC TGCCGCCAAT	1200
GTCCTCCGGG AAACATGGCT GATCTACAAA CACACAAAGC TGCTAAAGAA GATTGACCAC	1260
GCCAAAGTCA GGAAACACCA GAGGAAGTTC CTCCAAGCTA TTCACCAACT GAGGGGTGTC	1320
AAGATGGAAC AAAGGAAGCT GAGTGACCAA GCCAACACCC TGGTGGACCT TTCCAAGATG	1380
CAGAACGTCA TGTATGACTT GATCACGGAG CTCAACGACC GGAGTGAAGA CCTGGAAAAG	1440
CAGATTGGCA GCCTGGAATC CAAGCTGGAG CACCTCACAG CCAGCTTCAA TTCCCTGCCC	1500
CTGCTCATCG CAGACACCCT GCGCCAACAG CAGCAGCAGC TGCTCACTGC CTTCTGAGG	1560
GCCCCGGGCA TCAGTGTGGC TGTGGGAACT AGCCACGCCC CTCCCTCTGA CAGCCCTATC	1620
GGGATCAGCT CCACCTCTTT CCCGGAATTC CTAATATTC	1659

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu	Ser	Asp	Tyr	Ala	Leu	Ile	Phe	Gly	Met
1				5				10	

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln Arg Lys Phe Leu Gln Ala Ile His Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
 (B) LOCATION: 1..579
 (D) OTHER INFORMATION: /note= "human small conductance,
 calcium-activated potassium channel
 protein 2 (hSK2)"

(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 134..461
 (D) OTHER INFORMATION: /note= "core region of hSK2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ser Ser Cys Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn
 1 5 10 15

Leu Ser Ala Ser Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln
 20 25 30

Pro Leu Gln Pro Pro Ala Ser Val Gly Gly Gly Gly Ala Ser Ser
 35 40 45

Pro Ser Ala Ala Ala Ala Ala Ala Ala Val Ser Ser Ser Ala Pro
 50 55 60

Glu Ile Val Val Ser Lys Pro Glu His Asn Asn Ser Asn Asn Leu Ala
 65 70 75 80

Leu Tyr Gly Thr Gly Gly Gly Gly Ser Thr Gly Gly Gly Gly Gly Gly
 85 90 95

Gly Gly Ser Gly His Gly Ser Ser Ser Gly Thr Lys Ser Ser Lys Lys
 100 105 110
 Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His Arg Arg Ala Leu Phe
 115 120 125
 Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met Phe
 130 135 140
 Gly Ile Val Val Met Val Ile Glu Thr Glu Leu Ser Trp Gly Ala Tyr
 145 150 155 160
 Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu Lys Cys Leu Ile Ser Leu
 165 170 175
 Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Val Tyr His Ala Arg Glu
 180 185 190
 Ile Gln Leu Phe Met Val Asp Asn Gly Ala Asp Asp Trp Arg Ile Ala
 195 200 205
 Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys Leu Glu Ile Leu Val Cys
 210 215 220
 Ala Ile His Pro Ile Pro Gly Asn Tyr Thr Phe Thr Trp Thr Ala Arg
 225 230 235 240
 Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr Thr Ala Asp Val Asp Ile
 245 250 255
 Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val
 260 265 270
 Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile
 275 280 285
 Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr
 290 295 300
 Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser
 305 310 315 320
 Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr His
 325 330 335
 Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu Ile
 340 345 350
 Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro Asn Thr
 355 360 365
 Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly Ala Gly
 370 375 380
 Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu Leu Thr
 385 390 395 400
 Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln Leu Thr
 405 410 415

Lys Arg Val Lys Asn Ala Ala Ala Asn Val Leu Arg Glu Thr Trp Leu
 420 425 430
 Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys Ile Asp His Ala Lys Val
 435 440 445
 Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg Ser
 450 455 460
 Val Lys Met Glu Gln Arg Lys Leu Asn Asp Gln Ala Asn Thr Leu Val
 465 470 475 480
 Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr Asp Met Ile Ser Asp Leu
 485 490 495
 Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg Ile Val Thr Leu Glu Thr
 500 505 510
 Lys Leu Glu Thr Leu Ile Gly Ser Ile His Ala Leu Pro Gly Leu Ile
 515 520 525
 Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp Phe Ile Glu Ala Gln Met
 530 535 540
 Glu Ser Tyr Asp Lys His Val Thr Tyr Asn Ala Glu Arg Ser Arg Ser
 545 550 555 560
 Ser Ser Arg Arg Arg Arg Ser Ser Ser Thr Ala Pro Pro Thr Ser Ser
 565 570 575
 Glu Ser Ser

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..557
- (D) OTHER INFORMATION: /note= "N-terminally truncated form of human small conductance, calcium-activated potassium channel protein 3 (hSK3)"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 109..436
- (D) OTHER INFORMATION: /note= "core region of hSK3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Ser	Ser	Cys	Lys	Tyr	Ser	Gly	Gly	Val	Met	Lys	Pro	Leu	Ser	Arg	1	5	10	15
Leu	Ser	Ala	Ser	Arg	Arg	Asn	Leu	Ile	Glu	Ala	Glu	Thr	Glu	Gly	Gln	20	25	30	
Pro	Leu	Gln	Leu	Phe	Ser	Pro	Ser	Asn	Pro	Pro	Glu	Ile	Val	Ile	Ser	35	40	45	
Ser	Arg	Glu	Asp	Asn	His	Ala	His	Gln	Thr	Leu	Leu	His	His	Pro	Asn	50	55	60	
Ala	Thr	His	Asn	His	Gln	His	Ala	Gly	Thr	Thr	Ala	Ser	Ser	Thr	Thr	65	70	75	80
Phe	Pro	Lys	Ala	Asn	Lys	Arg	Lys	Asn	Gln	Asn	Ile	Gly	Tyr	Lys	Leu	85	90	95	
Gly	His	Arg	Arg	Ala	Leu	Phe	Glu	Lys	Arg	Lys	Arg	Leu	Ser	Asp	Tyr	100	105	110	
Ala	Leu	Ile	Phe	Gly	Met	Phe	Gly	Ile	Val	Val	Met	Val	Ile	Glu	Thr	115	120	125	
Glu	Leu	Ser	Trp	Gly	Leu	Tyr	Ser	Lys	Asp	Ser	Met	Phe	Ser	Leu	Ala	130	135	140	
Leu	Lys	Cys	Leu	Ile	Ser	Leu	Ser	Thr	Ile	Ile	Leu	Leu	Gly	Leu	Ile	145	150	155	160
Ile	Ala	Tyr	His	Thr	Arg	Glu	Val	Gln	Leu	Phe	Val	Ile	Asp	Asn	Gly	165	170	175	
Ala	Asp	Asp	Trp	Arg	Ile	Ala	Met	Thr	Tyr	Glu	Arg	Ile	Leu	Tyr	Ile	180	185	190	
Ser	Leu	Glu	Met	Leu	Val	Cys	Ala	Ile	His	Pro	Ile	Pro	Gly	Glu	Tyr	195	200	205	
Lys	Phe	Phe	Trp	Thr	Ala	Arg	Leu	Ala	Phe	Ser	Tyr	Thr	Pro	Ser	Arg	210	215	220	
Ala	Glu	Ala	Asp	Val	Asp	Ile	Ile	Leu	Ser	Ile	Pro	Met	Phe	Leu	Arg	225	230	235	240
Leu	Tyr	Leu	Ile	Ala	Arg	Val	Met	Leu	Leu	His	Ser	Lys	Leu	Phe	Thr	245	250	255	
Asp	Ala	Ser	Ser	Arg	Ser	Ile	Gly	Ala	Leu	Asn	Lys	Ile	Asn	Phe	Asn	260	265	270	
Thr	Arg	Phe	Val	Met	Lys	Thr	Leu	Met	Thr	Ile	Cys	Pro	Gly	Thr	Val	275	280	285	
Leu	Leu	Val	Phe	Ser	Ile	Ser	Leu	Trp	Ile	Ile	Ala	Ala	Trp	Thr	Val	290	295	300	
Arg	Val	Cys	Glu	Arg	Tyr	His	Asp	Gln	Gln	Asp	Val	Thr	Ser	Asn	Phe	305	310	315	320

Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr
 325 330 335
 Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu
 340 345 350
 Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val
 355 360 365
 Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe
 370 375 380
 Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn
 385 390 395 400
 Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys
 405 410 415
 Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln
 420 425 430
 Ala Ile His Gln Leu Arg Ser Val Lys Met Glu Gln Arg Lys Leu Ser
 435 440 445
 Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met
 450 455 460
 Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys
 465 470 475 480
 Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe
 485 490 495
 Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln
 500 505 510
 Gln Leu Leu Ser Ala Ile Ile Glu Ala Arg Gly Val Ser Val Ala Val
 515 520 525
 Gly Thr Thr His Thr Pro Ile Ser Asp Ser Pro Ile Gly Val Ser Ser
 530 535 540
 Thr Ser Phe Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys
 545 550 555

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1740 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1740

(D) OTHER INFORMATION: /note= "human small conductance,
calcium-activated potassium channel
protein 2 (hSK2) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGGCCGC TCAGCAACTT GAGCGCGTCC	60
CGCCGGAACC TGCACGAGAT GGA CTCAGAG GCGCAGCCCC TGCAGCCCCC CGCGTCTGTC	120
GGAGGAGGTG GCGGCGCGTC CTCCCCGTCT GCAGCCGCTG CCGCCGCCGC CGCTGTTTCG	180
TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCCGAGCACA ACAACTCCAA CAACCTGGCG	240
CTCTATGGAA CCGGCGGCGG AGGCAGCACT GGAGGAGGCG GCGGCGGTGG CGGGAGCGGG	300
CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG	360
CTGGGCCACC GCGCGCCCT GTTCGAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC	420
TTCGGCATGT TCGGCATCGT GGT CATGGTC ATCGAGACCG AGCTGTCGTG GGGCGCCTAC	480
GACAAGGCGT CGCTGTATT CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC	540
CTGCTCGGTC TGATCATCGT GTACCACGCC AGGGAAATAC AGTTGTTCAT GGTGGACAAT	600
GGAGCAGATG ACTGGAGAAT AGCCATGACT TATGAGCGTA TTTCTTCAT CTGCTTGGA	660
ATACTGGTGT GTGCTATTCA TCCCATACCT GGGAATTATA CATTACATG GACGGCCCCG	720
CTTGCCCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA	780
CCAATGTTCT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC	840
ACTGATGCCT CCTCTAGAAG CATTGGAGCA CTTAATAAGA TAAACTTCAA TACACGTTTT	900
GTTATGAAGA CTTTAATGAC TATATGCCCA GGAAGTGTAC TCTTGGTTTT TAGTATCTCA	960
TTATGGATAA TTGCCGCATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT	1020
GTTACTAGCA ACTTCCTTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT	1080
TATGGTGACA TGGTACCTAA CACATACTGT GGAAAAGGAG TCTGCTTACT TACTGGAATT	1140
ATGGGTGCTG GTTGCACAGC CCTGGTGGTA GCTGTAGTGG CAAGGAAGCT AGAACTTACC	1200
AAAGCAGAAA AACACGTGCA CAATTTTCATG ATGGATACTC AGCTGACTAA AAGAGTAAAA	1260
AATGCAGCTG CCAATGTACT CAGGGAAACA TGGCTAATTT AAAAAATAC AAAGCTAGTG	1320
AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTCAT	1380
CAATTAAGAA GTGTAAAAAT GGAACAGAGG AAAGTGAATG ACCAAGCAAA CACTTTGGTG	1440
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATTT CTGACTTAAA CGAAAGGAGT	1500
GAAGACTTCG AGAAGAGGAT TGTTACCCTG GAAACAAAAT TAGAGACTTT GATTGGTAGC	1560

ATCCACGCCC TCCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTTCATT 1620
 GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACCTACA ATGCTGAGCG GTCCCGGTCC 1680
 TCGTCCAGGA GGCGGCGGTC CTCTTCCACA GCACCACCAA CTTTCATCAGA GAGTAGCTAG 1740

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1674
- (D) OTHER INFORMATION: /note= "N-terminally truncated cDNA
for human small conductance,
calcium-activated potassium channel
protein 3 (hSK3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGCTCCT GCAAGTATAG CGGTGGGGTC ATGAAGCCCC TCAGCCGCCT CAGCGCCTCC 60
 CGGAGGAACC TCATCGAGGC CGAGACTGAG GGCCAACCCC TCCAGCTTTT CAGCCCTAGC 120
 AACCCCCCGG AGATCGTCAT CTCCTCCCGG GAGGACAACC ATGCCACCA GACCCTGCTC 180
 CATCACCTA ATGCCACCA CAACCACCAG CATGCCGGCA CCACCGCCAG CAGCACCACC 240
 TTCCCCAAAG CCAACAAGCG GAAAAACCAA AACATTGGCT ATAAGCTGGG ACACAGGAGG 300
 GCCCTGTTTG AAAAGAGAAA GCGACTGAGT GACTATGCTC TGATTTTGG GATGTTTGA 360
 ATTGTTGTTA TGGTGATAGA GACCGAGCTC TCTTGGGGTT TGTACTCAA GACTCCATG 420
 TTTTCGTTGG CCCTGAAATG CCTTATCAGT CTGTCCACCA TCATCCTTTT GGGCTTGATC 480
 ATCGCCTACC ACACACGTGA AGTCCAGCTC TTCGTGATCG ACAACGGCGC GGATGACTGG 540
 CGGATAGCCA TGACCTACGA GCGCATCCTC TACATCAGCC TGGAGATGCT GGTGTGCGCC 600
 ATCCACCCCA TTCCTGGCGA GTACAAGTTC TTCTGGACGG CACGCCTGGC CTTCTCCTAC 660
 ACACCCTCCC GGGCGGAGGC CGATGTGGAC ATCATCCTGT CTATCCCCAT GTTCCTGCGC 720
 CTGTACCTGA TCGCCGAGT CATGCTGCTG CACAGCAAGC TCTTCACCGA TGCCTCGTCC 780
 CGCAGCATCG GGGCCCTCAA CAAGATCAAC TTCAACACCC GCTTTGTCAT GAAGACGCTC 840
 ATGACCATCT GCCCTGGCAC TGTGCTGCTC GTGTTCAGCA TCTCTCTGTG GATCATTGCT 900
 GCCTGGACCG TCCGTGTCTG TGAAAGGTAC CATGACCAGC AGGACGTAAC TAGTAACTTT 960

CTGGGTGCCA TGTGGCTCAT CTCCATCACA TTCCTTTCCA TTGGTTATGG GGACATGGTG	1020
CCCCACACAT ACTGTGGGAA AGGTGTCTGT CTCCTCACTG GCATCATGGG TGCAGGCTGC	1080
ACTGCCCTTG TGGTGGCCGT GGTGGCCCGA AAGCTGGAAC TCACCAAAGC GGAGAAGCAC	1140
GTTCATAACT TCATGATGGA CACTCAGCTC ACCAAGCGGA TCAAGAATGC TGCAGCCAAT	1200
GTCCTTCGGG AAACATGGTT AATCTATAAA CACACAAAGC TGCTAAAGAA GATTGACCAT	1260
GCCAAAGTGA GGAAACACCA GAGGAAGTTC CTCCAAGCTA TCCACCAGTT GAGGAGCGTC	1320
AAGATGGAAC AGAGGAAGCT GAGTGACCAA GCCAACACTC TGGTGGACCT TTCCAAGATG	1380
CAGAATGTCA TGTATGACTT AATCACAGAA CTCAATGACC GGAGCGAAGA CCTGGAGAAG	1440
CAGATTGGCA GCCTGGAGTC GAAGCTGGAG CATCTCACCG CCAGCTTCAA CTCCCTGCCG	1500
CTGCTCATCG CCGACACCCT GCGCCAGCAG CAGCAGCAGC TCCTGTCTGC CATCATCGAG	1560
GCCCCGGGTG TCACGTGGC AGTGGGCACC ACCCACACC CAATCTCCGA TAGCCCCATT	1620
GGGGTCAGCT CCACCTCCTT CCCGACCCCG TACACAAGTT CAAGCAGTTG CTAA	1674

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAGCAGCT GCAGGTACAA CG

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGCTACTC TCTGATGAAG TTG

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGAGCTCCT GCAAGTATAG C

21

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTAGCAACTG CTTGAAC TTG TG

22

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..328
- (D) OTHER INFORMATION: /note= "core region of hSK1 from
amino acid positions 124 through 451"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met Phe Gly Ile Val Val Met
1 5 10 15

Val Thr Glu Thr Glu Leu Ser Trp Gly Val Tyr Thr Lys Glu Ser Leu
20 25 30

Tyr Ser Phe Ala Leu Lys Cys Leu Ile Ser Leu Ser Thr Ala Ile Leu
35 40 45

Leu Gly Leu Val Val Leu Tyr His Ala Arg Glu Ile Gln Leu Phe Met
 50 55 60
 Val Asp Asn Gly Ala Asp Asp Trp Arg Ile Ala Met Thr Cys Glu Arg
 65 70 75 80
 Val Phe Leu Ile Ser Leu Glu Leu Ala Val Cys Ala Ile His Pro Val
 85 90 95
 Pro Gly His Tyr Arg Phe Thr Trp Thr Ala Arg Leu Ala Phe Thr Tyr
 100 105 110
 Ala Pro Ser Val Ala Glu Ala Asp Val Asp Val Leu Leu Ser Ile Pro
 115 120 125
 Met Phe Leu Arg Leu Tyr Leu Leu Gly Arg Val Met Leu Leu His Ser
 130 135 140
 Lys Ile Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys
 145 150 155 160
 Ile Thr Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys
 165 170 175
 Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Ser Trp Ile Ile Ala
 180 185 190
 Ala Trp Thr Val Arg Val Cys Glu Arg Tyr His Asp Lys Gln Glu Val
 195 200 205
 Thr Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu
 210 215 220
 Ser Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly
 225 230 235 240
 Val Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val
 245 250 255
 Val Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His
 260 265 270
 Val His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn
 275 280 285
 Ala Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr
 290 295 300
 Arg Leu Val Lys Lys Pro Asp Gln Ala Arg Val Arg Lys His Gln Arg
 305 310 315 320
 Lys Phe Leu Gln Ala Ile His Gln
 325

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gly	His	Arg	Arg	Ala	Leu	Phe	Glu	Lys	Arg	Lys	Arg	Leu	Ser	Asp	Tyr
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Phe	Thr	Asp	Ala	Ser	Ser	Arg	Ser	Ile	Gly	Ala	Leu
1				5				10			

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala	Arg	Lys	Leu	Glu	Leu	Thr	Lys	Ala	Glu	Lys	His	Val	His	Asn	Phe
1				5				10						15	

Met	Met	Asp	Thr	Gln	Leu	Thr	Lys	Arg
				20				25

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1287

(D) OTHER INFORMATION: /note= "human intermediate
conductance, calcium-activated
potassium channel protein 1
(hIK1) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGGCGGGG ATCTGGTGCT TGGCCTGGGG GCCTTGAGAC GCCGAAAGCG CTTGCTGGAG	60
CAGGAGAAGT CTCTGGCCGG CTGGGCACTG GTGCTGGCAG GAACTGGCAT TGGACTCATG	120
GTGCTGCATG CAGAGATGCT GTGGTTCGGG GGGTGCTCGT GGGCGCTCTA CCTGTTCTTG	180
GTAAATGCA CGATCAGCAT TTCCACCTTC TTAACCTCT GCCTCATCGT GGCTTTTCAT	240
GCCAAAGAGG TCCAGCTGTT CAGTACCGAC AACGGGCTGC GGGACTGGCG CGTGGTGCTC	300
CTGACCGGGC GGCAGGCGGC GCAGATCGTG CTGGAGCTGG TGGTGTGTGG GCTGCACCCG	360
GCGCCCGTGC GGGGCCCCGCC GTGCGTGCA GATTTAGGGG CGCCGCTGAC CTCCCCGCAG	420
CCCTGGCCGG GATTCTTGGG CCAAGGGGAA GCGCTGCTGT CCCTGGCCAT GCTGCTGCGT	480
CTCTACCTGG TGCCCCGCGC CGTGCTCCTG CGCAGCGGCG TCCTGCTCAA CGCTTCCTAC	540
CGCAGCATCG GCGCTCTCAA TCAAGTCCGC TTCCGCCACT GGTTCGTGGC CAAGCTTTAC	600
ATGAACACGC ACCCTGGCCG CCTGCTGCTC GGCCTCACGC TTGGCCTCTG GCTGACCACC	660
GCCTGGGTGC TGTCCGTGGC CGAGAGGCAG GCTGTTAATG CCACTGGGCA CCTTTCAGAC	720
ACACTTTGGC TGATCCCCAT CACATTCTTG ACCATCGGCT ATGGTGACGT GGTGCCGGGC	780
ACCATGTTGG GCAAGATCGT CTGCCTGTGC ACTGGAGTCA TGGGTGTCTG CTGCACAGCC	840
CTGCTGGTGG CCGTGGTGGC CCGGAAGCTG GAGTTTAACA AGGCAGAGAA GCACGTGCAC	900
AACTTCATGA TGGATATCCA GAATACCAA GAGATGAAGG AGTCCGCTGC CCGAGTGCTA	960
CAAGAAGCCT GGATGTTCTA CAAACATACT CGCAGGAAGG AGTCTCATGC TGCCCCGAGG	1020
CATCAGCGCA AGCTGCTGGC CGCCATCAAC GCGTTCCGCC AGGTGCGGCT GAAACACCGG	1080
AAGCTCCGGG AACAAAGTGA CTCCATGGTG GACATCTCCA AGATGCACAT GATCCTGTAT	1140
GACCTGCAGC AGAATCTGAG CAGCTCACAC CGGGCCCTGG AGAAACAGAT TGACACGCTG	1200
GCGGGGAAGC TGGATGCCCT GACTGAGCTG CTTAGCACTG CCCTGGGGCC GAGGCAGCTT	1260
CCAGAACCCA GCCAGCAGTC CAAGTAG	1287

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: /note= "human intermediate conductance, calcium-activated potassium channel protein 1 (hIK1)"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 25..351
- (D) OTHER INFORMATION: /note= "core region of hIK1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg Lys
1           5           10           15
Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu
20           25           30
Ala Gly Thr Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp
35           40           45
Phe Gly Gly Cys Ser Trp Ala Leu Tyr Leu Phe Leu Val Lys Cys Thr
50           55           60
Ile Ser Ile Ser Thr Phe Leu Leu Leu Cys Leu Ile Val Ala Phe His
65           70           75           80
Ala Lys Glu Val Gln Leu Phe Ser Thr Asp Asn Gly Leu Arg Asp Trp
85           90           95
Arg Val Val Leu Leu Thr Gly Arg Gln Ala Ala Gln Ile Val Leu Glu
100          105          110
Leu Val Val Cys Gly Leu His Pro Ala Pro Val Arg Gly Pro Pro Cys
115          120          125
Val Gln Asp Leu Gly Ala Pro Leu Thr Ser Pro Gln Pro Trp Pro Gly
130          135          140
Phe Leu Gly Gln Gly Glu Ala Leu Leu Ser Leu Ala Met Leu Leu Arg
145          150          155          160
Leu Tyr Leu Val Pro Arg Ala Val Leu Leu Arg Ser Gly Val Leu Leu
165          170          175
Asn Ala Ser Tyr Arg Ser Ile Gly Ala Leu Asn Gln Val Arg Phe Arg
180          185          190

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His	Trp	Phe	Val	Ala	Lys	Leu	Tyr	Met	Asn	Thr	His	Pro	Gly	Arg	Leu
		195					200					205			
Leu	Leu	Gly	Leu	Thr	Leu	Gly	Leu	Trp	Leu	Thr	Thr	Ala	Trp	Val	Leu
		210				215					220				
Ser	Val	Ala	Glu	Arg	Gln	Ala	Val	Asn	Ala	Thr	Gly	His	Leu	Ser	Asp
225					230					235					240
Thr	Leu	Trp	Leu	Ile	Pro	Ile	Thr	Phe	Leu	Thr	Ile	Gly	Tyr	Gly	Asp
				245					250					255	
Val	Val	Pro	Gly	Thr	Met	Leu	Gly	Lys	Ile	Val	Cys	Leu	Cys	Thr	Gly
			260					265					270		
Val	Met	Gly	Val	Cys	Cys	Thr	Ala	Leu	Leu	Val	Ala	Val	Val	Ala	Arg
		275					280					285			
Lys	Leu	Glu	Phe	Asn	Lys	Ala	Glu	Lys	His	Val	His	Asn	Phe	Met	Met
	290					295					300				
Asp	Ile	Gln	Asn	Thr	Lys	Glu	Met	Lys	Glu	Ser	Ala	Ala	Arg	Val	Leu
305					310					315					320
Gln	Glu	Ala	Trp	Met	Phe	Tyr	Lys	His	Thr	Arg	Arg	Lys	Glu	Ser	His
				325					330					335	
Ala	Ala	Arg	Arg	His	Gln	Arg	Lys	Leu	Leu	Ala	Ala	Ile	Asn	Ala	Phe
			340					345					350		
Arg	Gln	Val	Arg	Leu	Lys	His	Arg	Lys	Leu	Arg	Glu	Gln	Val	Asn	Ser
		355					360					365			
Met	Val	Asp	Ile	Ser	Lys	Met	His	Met	Ile	Leu	Tyr	Asp	Leu	Gln	Gln
	370					375					380				
Asn	Leu	Ser	Ser	Ser	His	Arg	Ala	Leu	Glu	Lys	Gln	Ile	Asp	Thr	Leu
385					390					395					400
Ala	Gly	Lys	Leu	Asp	Ala	Leu	Thr	Glu	Leu	Leu	Ser	Thr	Ala	Leu	Gly
				405					410					415	
Pro	Arg	Gln	Leu	Pro	Glu	Pro	Ser	Gln	Gln	Ser	Lys				
			420					425							

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val	Arg	Gly	Pro	Pro	Cys	Val	Gln	Asp	Leu	Gly	Ala	Pro	Leu	Thr	Ser
1				5					10					15	

Pro Gln Pro Trp Pro Gly Phe Leu Gly Gln Gly Glu Ala Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGTGCGTG CAGGATTTAG G

21

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAGAGGCCA AGCGTGAGGC C

21

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TCCAAGATGC ACATGATCCT G

21

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGACTGCTGG CTGGGTTCTG G

21

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGGGCGGGG ATCTGGTGCT TG

22

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTACTTGGAC TGCTGGCTGG GTTC

24

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGGCGGGG ATCTGGTGCT TGG

23

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGTCCAGCT ACTTGGACTG CTG

23

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ala	Arg	Lys	Leu	Glu	Leu	Thr	Lys	Ala	Glu	Lys	His	Val	His	Asn	Phe
1				5					10					15	

Met	Met	Asp	Thr	Gln	Leu	Thr	Lys
				20			

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..732
- (D) OTHER INFORMATION: /note= "full-length rat small conductance, calcium-activated potassium channel protein 3 (rSK3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Asp	Thr	Ser	Gly	His	Phe	His	Glu	Ser	Gly	Val	Gly	Asp	Leu	Asp
1				5					10					15	

Glu	Asp	Pro	Lys	Cys	Pro	Cys	Pro	Ser	Ser	Gly	Asp	Glu	Gln	Gln	Gln
			20					25					30		

Gln	Gln	Gln	Pro	Pro	Pro	Pro	Ser	Ala	Pro	Pro	Ala	Val	Pro	Gln	Gln
			35				40					45			

Pro	Pro	Gly	Pro	Leu	Leu	Gln	Pro	Gln	Pro	Pro	Gln	Leu	Gln	Gln	Gln
			50			55						60			

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Ala Pro Leu His Pro Leu Pro Gln Leu Ala Gln Leu Gln Ser Gln Val
 85 90 95
 Val His Pro Gly Leu Leu His Ser Ser Pro Thr Ala Phe Arg Ala Pro
 100 105 110
 Asn Ser Ala Asn Ser Thr Ala Ile Leu His Pro Ser Ser Arg Gln Gly
 115 120 125
 Ser Gln Leu Asn Leu Asn Asp His Leu Val Gly His Ser Pro Ser Ser
 130 135 140
 Thr Ala Thr Ser Gly Pro Gly Gly Gly Ser Arg His Arg Gln Ala Ser
 145 150 155 160
 Pro Val Val His Arg Arg Asp Ser Asn Pro Phe Thr Glu Ile Ala Met
 165 170 175
 Ser Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro Leu Ser Arg Leu
 180 185 190
 Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Pro Glu Gly Gln Pro
 195 200 205
 Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Ile Ile Ser Ser
 210 215 220
 Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro Asn Ala
 225 230 235 240
 Thr His Asn His Gln His Ala Gly Thr Thr Ala Gly Ser Thr Thr Phe
 245 250 255
 Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly
 260 265 270
 His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala
 275 280 285
 Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu
 290 295 300
 Leu Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe Ser Leu Ala Leu
 305 310 315 320
 Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile
 325 330 335
 Ala Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile Asp Asn Gly Ala
 340 345 350
 Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Leu Tyr Ile Ser
 355 360 365
 Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu Tyr Lys
 370 375 380

Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg Ala
 385 390 395 400
 Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu
 405 410 415
 Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp
 420 425 430
 Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr
 435 440 445
 Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu
 450 455 460
 Leu Met Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg
 465 470 475 480
 Val Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu
 485 490 495
 Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly
 500 505 510
 Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr
 515 520 525
 Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala
 530 535 540
 Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met
 545 550 555 560
 Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn Val
 565 570 575
 Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys
 580 585 590
 Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala
 595 600 605
 Ile His Gln Leu Arg Gly Val Lys Met Glu Gln Arg Lys Leu Ser Asp
 610 615 620
 Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met Tyr
 625 630 635 640
 Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys Gln
 645 650 655
 Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe Asn
 660 665 670
 Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln Gln
 675 680 685
 Leu Leu Thr Ala Phe Val Glu Ala Arg Gly Ile Ser Val Ala Val Gly
 690 695 700

Thr Ser His Ala Pro Pro Ser Asp Ser Pro Ile Gly Ile Ser Ser Thr
705 710 715 720

Ser Phe Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys
725 730

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2224
- (D) OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 3 (rSK3) full-length cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CATGGACACT TCTGGGCACT TCCATGAGTC GGGGGTGGGG GATCTGGATG AAGACCCCAA	60
GTGTCCCTGT CCATCTTCTG GGGACGAGCA ACAGCAGCAA CAGCAACCGC CACCACCGTC	120
AGCGCCACCA GCAGTCCCCC AGCAGCCTCC GGGACCCTTG CTGCAGCCTC AGCCTCCGCA	180
GCTTCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA	240
GGCTCCACTG CACCCCCTGC CTCAGCTTGC CCAACTCCAG AGCCAGGTTG TCCATCCTGG	300
TCTGTTGCAC TCTTCTCCCA CGGCTTTCAG GGCTCCCAAT TCAGCCAACT CCACCGCCAT	360
CCTCCACCCT TCCTCCAGGC AAGGCAGCCA GCTAAATCTC AATGACCACT TGGTTGGCCA	420
CTCTCCAAGT TCCACAGCCA CAAGTGGGCC TGGTGGAGGC AGCCGGCACC GGCAGGCCAG	480
CCCCGTGGTG CACCGGCGGG ACAGCAATCC CTTACGGAG ATAGCTATGA GTCCTGCAA	540
ATACAGCGGT GGGGTCATGA AGCCCCTCAG CCGCCTCAGC GCCTCTCGGA GAAACCTTAT	600
CGAGGCCGAG CCTGAGGGCC AACCCTCCA GCTCTTCAGT CCCAGCAACC CCCAGAGAT	660
TATCATCTCC TCCAGGGAGG ATAACCATGC CCACCAGACT CTGCTCCATC ACCCAACGC	720
TACCCACAAC CACCAGCATG CCGGCACCAC TGCTGGCAGC ACCACCTTCC CCAAAGCCAA	780
CAAGCGGAAA AACCAAAACA TTGGCTATAA GCTGGGGCAC AGGAGGGCCC TGTTTGAAAA	840
GAGAAAGCGA CTGAGTGACT ATGCTCTGAT TTTTGGGATG TTTGGAATTG TTGTTATGGT	900
GATAGAGACC GAACTGTCTT GGGGTTTGTA CTCAAAGGAT TCCATGTTTT CGTTGGCCCT	960
GAAATGCCTT ATCAGTTTAT CCACCATCAT CCTGCTTGGT TTGATCATCG CCTACCACAC	1020

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AAGGGAAGTA CAGCTCTTTG TGATCGACAA TGGTGCAGAT GACTGGCGGA TAGCCATGAC 1080
CTATGAGCGC ATCCTCTACA TCAGCCTGGA GATGCTGGTG TCGGCCATCC ACCCCATTCC 1140
TGGAGAGTAC AAGTTCTTCT GGACGGCACG CCTGGCCTTC TCCTACACCC CCTCTCGGGC 1200
AGAGGCTGAC GTGGACATTA TTCTGTCCAT CCCCATGTTC TTGCGCCTAT ACCTGATCGC 1260
CCGAGTCATG CTGCTACATA GCAAGCTCTT CACGGATGCC TCATCCCGAA GCATCGGGGC 1320
CCTCAACAAG ATCAACTTCA ACACCCGATT CGTCATGAAG ACGCTCATGA CCATCTGCCC 1380
GGGCACGGTG CTGCTAATGT TCAGCATCTC TCTGTGGATC ATCGCTGCCT GGACTGTGAG 1440
AGTCTGTGAA AGGTACCATG ACCAGCAGGA CGTAACTAGT AACTTTCTGG GTGCCATGTG 1500
GCTCATCTCC ATCACGTTCC TTTCATTGG CTATGGGGAC ATGGTGCCCC ACACATACTG 1560
TGGGAAAGGT GTCTGTCTTC TCACTGGCAT CATGGGTGCA GGCTGCACTG CCCTCGTGGT 1620
AGCTGTGGTT GCCCGGAAGC TCGAACTCAC CAAAGCAGAG AAGCATGTGC ACAACTTCAT 1680
GATGGACACT CAGCTCACCA AACGGATCAA GAACGCTGCC GCCAATGTCC TCCGGGAAAC 1740
ATGGCTGATC TACAAACACA CAAAGCTGCT AAAGAAGATT GACCACGCCA AAGTCAGGAA 1800
ACACCAGAGG AAGTTCTCTC AAGCTATTCA CCAACTGAGG GGTGTCAAGA TGGAACAAAG 1860
GAAGCTGAGT GACCAAGCCA ACACCCTGGT GGACCTTTCC AAGATGCAGA ACGTCATGTA 1920
TGACTTGATC ACGGAGCTCA ACGACCGGAG TGAAGACCTG GAAAAGCAGA TTGGCAGCCT 1980
GGAATCCAAG CTGGAGCACC TCACAGCCAG CTTCAATTCC CTGCCCCTGC TCATCGCAGA 2040
CACCCTGCGC CAACAGCAGC AGCAGCTGCT CACTGCCTTC GTGGAGGCCC GGGGCATCAG 2100
TGTGGCTGTG GGAAGTAGCC ACGCCCCTCC CTCTGACAGC CCTATCGGGA TCAGCTCCAC 2160
CTCTTTCCCA ACCCCATACA CAAGTTCAAG CAGTTGCTAA ATAAACTCC CCACTCCAGA 2220
AGCA 2224

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(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Phe Xaa Ser Ile Pro Xaa Xaa Xaa Trp Trp Ala Xaa Val Thr Met Thr
1           5           10           15
Thr Val Gly Tyr Gly Asp Met Xaa Pro
20           25

```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asn Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..736
- (D) OTHER INFORMATION: /note= "full length human small
conductance, calcium-activated
potassium channel protein 3 (hSK3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Asp	Thr	Ser	Gly	His	Phe	His	Asp	Ser	Gly	Val	Gly	Asp	Leu	Asp	1	5	10	15
Glu	Asp	Pro	Lys	Cys	Pro	Cys	Pro	Ser	Ser	Gly	Asp	Glu	Gln	Gln	Gln	20	25	30	
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Pro	Ala	Pro	Pro	35	40	45	
Ala	Ala	Pro	Gln	Gln	Pro	Leu	Gly	Pro	Ser	Leu	Gln	Pro	Gln	Pro	Pro	50	55	60	
Gln	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	65	70	75	80

Gln Gln Gln Gln Gln Pro Pro His Pro Leu Ser Gln Leu Ala Gln Leu
 85 90 95
 Gln Ser Gln Pro Val His Pro Gly Leu Leu His Ser Ser Pro Thr Ala
 100 105 110
 Phe Arg Ala Pro Pro Ser Ser Asn Ser Thr Ala Ile Leu His Pro Ser
 115 120 125
 Ser Arg Gln Gly Ser Gln Leu Asn Leu Asn Asp His Leu Leu Gly His
 130 135 140
 Ser Pro Ser Ser Thr Ala Thr Ser Gly Pro Gly Gly Gly Ser Arg His
 145 150 155 160
 Arg Gln Ala Ser Pro Leu Val His Arg Arg Asp Ser Asn Pro Ser Thr
 165 170 175
 Glu Ile Ala Met Ser Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro
 180 185 190
 Leu Ser Arg Leu Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Thr
 195 200 205
 Glu Gly Gln Pro Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile
 210 215 220
 Val Ile Ser Ser Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His
 225 230 235 240
 His Pro Asn Ala Thr His Asn His Gln His Ala Gly Thr Thr Ala Ser
 245 250 255
 Ser Thr Thr Phe Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly
 260 265 270
 Tyr Lys Leu Gly His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu
 275 280 285
 Ser Asp Tyr Ala Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val
 290 295 300
 Ile Glu Thr Glu Leu Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe
 305 310 315 320
 Ser Leu Ala Leu Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu
 325 330 335
 Gly Leu Ile Ile Ala Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile
 340 345 350
 Asp Asn Gly Ala Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile
 355 360 365
 Leu Tyr Ile Ser Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro
 370 375 380
 Gly Glu Tyr Lys Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr
 385 390 395 400

Pro Ser Arg Ala Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met
 405 410 415
 Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys
 420 425 430
 Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile
 435 440 445
 Asn Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro
 450 455 460
 Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala
 465 470 475 480
 Trp Thr Val Arg Val Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr
 485 490 495
 Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser
 500 505 510
 Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val
 515 520 525
 Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val
 530 535 540
 Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val
 545 550 555 560
 His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala
 565 570 575
 Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys
 580 585 590
 Leu Leu Lys Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys
 595 600 605
 Phe Leu Gln Ala Ile His Gln Leu Arg Ser Val Lys Met Glu Gln Arg
 610 615 620
 Lys Leu Ser Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln
 625 630 635 640
 Asn Val Met Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp
 645 650 655
 Leu Glu Lys Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr
 660 665 670
 Ala Ser Phe Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln
 675 680 685
 Gln Gln Gln Gln Leu Leu Ser Ala Ile Ile Glu Ala Arg Gly Val Ser
 690 695 700
 Val Ala Val Gly Thr Thr His Thr Pro Ile Ser Asp Ser Pro Ile Gly
 705 710 715 720

Val Ser Ser Thr Ser Phe Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys
 725 730 735

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2462
- (D) OTHER INFORMATION: /note= "human small conductance,
calcium-activated potassium channel
protein 3 (hSK3) full length cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTTCTTTCA CCCCTCTTC TTTCTCCAAG CTCCCCTCCT GCTCTCCCTC CCTGCCCAAT	60
ACAATGCATT CTTGAGTGGC AGCGTCTGGA CTCCAGGCAG CCCAGAGAA CCGAAGCAAG	120
CCAAAGAGAG GACTGGAGCC AAGATACTGG TGGGGGAGAT TGGATGCCTG GCTTTCTTTG	180
AGGACATCTT TGGAGCGAGG GTGGCTTTGG GGTGGGGGCT TGTGCTGCAG GGAATACAGC	240
CAGGCCCCAA GATGGACACT TCTGGGCACT TCCATGACTC GGGGGTGGGG GACTTGGATG	300
AAGACCCCAA GTGCCCTGT CCATCCTCTG GGGATGAGCA GCAGCAGCAG CAGCAGCAGC	360
AACAGCAGCA GCAGCCACCA CCGCCAGCGC CACCAGCAGC CCCCAGCAG CCCCTGGGAC	420
CCTCGCTGCA GCCTCAGCCT CCGCAGCTTC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC	480
AGCAGCAGCA GCAGCAGCAG CAGCAGCCAC CGCATCCCCCT GTCTCAGCTC GCCCAACTCC	540
AGAGCCAGCC CGTCCACCCT GGCCTGCTGC ACTCCTCTCC CACCGCTTTC AGGGCCCCCC	600
CTTCGTCCAA CTCCACCGCC ATCCTCCACC CTTCTCCAG GCAAGGCAGC CAGCTCAATC	660
TCAATGACCA CTTGCTTGGC CACTCTCCAA GTTCCACAGC TACAAGTGGG CCTGGCGGAG	720
GCAGCCGGCA CCGACAGGCC AGCCCCCTGG TGCACCGGCG GGACAGCAAC CCCTCCACGG	780
AGATCGCCAT GAGCTCCTGC AAGTATAGCG GTGGGGTCAT GAAGCCCCCTC AGCCGCCTCA	840
GCGCCTCCCG GAGGAACCTC ATCGAGGCCG AGACTGAGGG CCAACCCCTC CAGCTTTTCA	900
GCCCTAGCAA CCCCCGGAG ATCGTCATCT CCTCCGGGA GGACAACCAT GCCCACCAGA	960
CCCTGCTCCA TCACCCTAAT GCCACCCACA ACCACCAGCA TGCCGGCACC ACCGCCAGCA	1020
GCACCACCTT CCCCAAAGCC AACAAGCGGA AAAACCAAAA CATTGGCTAT AAGCTGGGAC	1080

ACAGGAGGGC CCTGTTTGAA AAGAGAAAGC GACTGAGTGA CTATGCTCTG ATTTTTGGGA 1140
 TGTTTGGAAT TGTTGTTATG GTGATAGAGA CCGAGCTCTC TTGGGGTTTG TACTCAAAGG 1200
 ACTCCATGTT TTCGTTGGCC CTGAAATGCC TTATCAGTCT GTCCACCATC ATCCTTTTGG 1260
 GCTTGATCAT CGCCTACCAC ACACGTGAAG TCCAGCTCTT CGTGATCGAC AACGGCGCGG 1320
 ATGACTGGCG GATAGCCATG ACCTACGAGC GCATCCTCTA CATCAGCCTG GAGATGCTGG 1380
 TGTGCGCCAT CCACCCCATC CCTGGCGAGT ACAAGTTCTT CTGGACGGCA CGCCTGGCCT 1440
 TCTCCTACAC ACCCTCCCGG GCGGAGGCCG ATGTGGACAT CATCCTGTCT ATCCCCATGT 1500
 TCCTGCGCCT GTACCTGATC GCCCGAGTCA TGCTGCTGCA CAGCAAGCTC TTCACCGATG 1560
 CCTCGTCCCG CAGCATCGGG GCCCTCAACA AGATCAACTT CAACACCCGC TTTGTCATGA 1620
 AGACGCTCAT GACCATCTGC CCTGGCACTG TGCTGCTCGT GTTCAGCATC TCTCTGTGGA 1680
 TCATTGCTGC CTGGACCGTC CGTGTCTGTG AAAGGTACCA TGACCAGCAG GACGTAACCTA 1740
 GTAACCTTCT GGGTGCCATG TGGCTCATCT CCATCACATT CCTTTCCATT GGTATGGGG 1800
 ACATGGTGCC CCACACATAC TGTGGGAAAG GTGTCTGTCT CCTCACTGGC ATCATGGGTG 1860
 CAGGCTGCAC TGCCCTTGTC GTGGCCGTGG TGGCCCGAAA GCTGGAAGTC ACCAAAGCGG 1920
 AGAAGCACGT TCATAACTTC ATGATGGACA CTCAGCTCAC CAAGCGGATC AAGAATGCTG 1980
 CAGCCAATGT CCTTCGGGAA ACATGGTTAA TCTATAAACA CACAAAGCTG CTAAAGAAGA 2040
 TTGACCATGC CAAAGTGAGG AAACACCAGA GGAAGTTCCT CCAAGCTATC CACCAGTTGA 2100
 GGAGCGTCAA GATGGAACAG AGGAAGCTGA GTGACCAAGC CAACACTCTG GTGGACCTTT 2160
 CCAAGATGCA GAATGTCATG TATGACTTAA TCACAGAACT CAATGACCGG AGCGAAGACC 2220
 TGGAGAAGCA GATTGGCAGC CTGGAGTCGA AGCTGGAGCA TCTCACC GCC 2280
 CCCTGCCGCT GCTCATCGCC GACACCCTGC GCCAGCAGCA GCAGCAGCTC CTGTCTGCCA 2340
 TCATCGAGGC CCGGGGTGTC AGCGTGGCAG TGGGCACCAC CCACACCCCA ATCTCCGATA 2400
 GCCCCATTGG GGTGAGCTCC ACCTCCTTCC CGACCCCGTA CACAAGTTCA AGCAGTTGCT 2460
 AA 2462

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